

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/643,836

Source: _____

Date Processed by STIC: _____

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RAW SEQUENCE LISTING

DATE: 01/11/2005

PATENT APPLICATION: US/10/643,836

TIME: 12:22:35

Input Set : N:\Crf3\RULE60\10643836.RAW.txt

Output Set: N:\CRF4\01112005\J643836.raw

```

1 <110> APPLICANT: Dumas Milne Edwards, Jean Baptiste
2      Bougueleret, Lydie
3      Jobert, Severin
4 <120> TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED
PROTEINS
5 <130> FILE REFERENCE: 78.US3.REG
6 <140> CURRENT APPLICATION NUMBER: 10/643,836
7 <141> CURRENT FILING DATE: 2003-08-19
8 <150> PRIOR APPLICATION NUMBER: US/09/731,872
9 <151> PRIOR FILING DATE: 2000-12-07
10 <150> PRIOR APPLICATION NUMBER: US 60/169,629
11 <151> PRIOR FILING DATE: 1999-12-08
12 <150> PRIOR APPLICATION NUMBER: US 60/187,470
13 <151> PRIOR FILING DATE: 2000-03-06
14 <160> NUMBER OF SEQ ID NOS: 482
15 <170> SOFTWARE: Patent.pm
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2201
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: 169..1692
24 <221> NAME/KEY: sig_peptide
25 <222> LOCATION: 169..249
26 <223> OTHER INFORMATION: Von Heijne matrix
27      score 7.15265901862021
28      seq VLLLLLLERGMFS/SP
W--> 29 <400> 1
30      agatgtgaat agctccacta taccagcctc gtcttccttc cgggggacaa cgtggggtcag      60
31      ggcacagaga gatatttaat gtcaccctct tggggctttc atgggactcc ctctgccaca      120
32      ttttttgag gttgggaaag ttgctagagg cttcagaact ccagccta atg gat ccc      177
33                                     Met Asp Pro
34                                     -25
35      aaa ctc ggg aga atg gct gcg tcc ctg ctg gct gtg ctg ctg ctg ctg      225
36      Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu Leu Leu Leu
37                                     -20      -15      -10
38      ctg ctg gag cgc ggc atg ttc tcc tca ccc tcc ccg ccc ccg gcg ctg      273
39      Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro Ala Leu
40                                     -5      1      5
41      tta gag aaa gtc ttc cag tac att gac ctc cat cag gat gaa ttt gtg      321
42      Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp Glu Phe Val
43      10      15      20
44      cag acg ctg aag gag tgg gtg gcc atc gag agc gac tct gtc cag cct      369

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45	Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro	
46	25 30 35 40	
47	gtg cct cgc ttc aga caa gag ctc ttc aga atg atg gcc gtg gct gcg	417
48	Val Pro Arg Phe Arg Gln Glu Leu Phe Arg Met Met Ala Val Ala Ala	
49	45 50 55	
50	gac acg ctg cag cgc ctg ggg gcc cgt gtg gcc tcg gtg gac atg ggt	465
51	Asp Thr Leu Gln Arg Leu Gly Ala Arg Val Ala Ser Val Asp Met Gly	
52	60 65 70	
53	cct cag cag ctg ccc gat ggt cag agt ctt cca ata cct ccc gtc atc	513
54	Pro Gln Gln Leu Pro Asp Gly Gln Ser Leu Pro Ile Pro Pro Val Ile	
55	75 80 85	
56	ctg gcc gaa ctg ggg agc gat ccc acg aaa ggc acc gtg tgc ttc tac	561
57	Leu Ala Glu Leu Gly Ser Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr	
58	90 95 100	
59	ggc cac ttg gac gtg cag cct gct gac cgg ggc gat ggg tgg ctc acg	609
60	Gly His Leu Asp Val Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr	
61	105 110 115 120	
62	gac ccc tat gtg ctg acg gag gta gac ggg aaa ctt tat gga cga gga	657
63	Asp Pro Tyr Val Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly	
64	125 130 135	
65	gcg acc gac aac aaa ggc cct gtc ttg gct tgg atc aat gct gtg agc	705
66	Ala Thr Asp Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser	
67	140 145 150	
68	gcc ttc aga gcc ctg gag caa gat ctt cct gtg aat atc aaa ttc atc	753
69	Ala Phe Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile	
70	155 160 165	
71	att gag ggg atg gaa gag gct ggc tct gtt gcc ctg gag gaa ctt gtg	801
72	Ile Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val	
73	170 175 180	
74	gaa aaa gaa aag gac cga ttc ttc tct ggt gtg gac tac att gta att	849
75	Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val Ile	
76	185 190 195 200	
77	tca gat aac ctg tgg atc agc caa agg aag cca gca atc act tat gga	897
78	Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr Tyr Gly	
79	205 210 215	
80	acc cgg ggg aac agc tac ttc atg gtg gag gtg aaa tgc aga gac cag	945
81	Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys Arg Asp Gln	
82	220 225 230	
83	gat ttt cac tca gga acc ttt ggt ggc atc ctt cat gaa cca atg gct	993
84	Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His Glu Pro Met Ala	
85	235 240 245	
86	gat ctg gtt gct ctt ctc ggt agc ctg gta gac tcg tct ggt cat atc	1041
87	Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp Ser Ser Gly His Ile	
88	250 255 260	
89	ctg gtc cct gga atc tat gat gaa gtg gtt cct ctt aca gaa gag gaa	1089
90	Leu Val Pro Gly Ile Tyr Asp Glu Val Val Pro Leu Thr Glu Glu Glu	
91	265 270 275 280	
92	ata aat aca tac aaa gcc atc cat cta gac cta gaa gaa tac cgg aat	1137
93	Ile Asn Thr Tyr Lys Ala Ile His Leu Asp Leu Glu Glu Tyr Arg Asn	

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Input Set : N:\Crf3\RULE60\10643836.RAW.txt

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94          285          290          295
95    agc agc cgg gtt gag aaa ttt ctg ttc gat act aag gag gag att cta    1185
96    Ser Ser Arg Val Glu Lys Phe Leu Phe Asp Thr Lys Glu Glu Ile Leu
97          300          305          310
98    atg cac ctc tgg agg tac cca tct ctt tct att cat ggg atc gag ggc    1233
99    Met His Leu Trp Arg Tyr Pro Ser Leu Ser Ile His Gly Ile Glu Gly
100          315          320          325
101    gcg ttt gat gag cct gga act aaa aca gtc ata cct ggc cga gtt ata    1281
102    Ala Phe Asp Glu Pro Gly Thr Lys Thr Val Ile Pro Gly Arg Val Ile
103          330          335          340
104    gga aaa ttt tca atc cgt cta gtc cct cac atg aat gtg tct gcg gtg    1329
105    Gly Lys Phe Ser Ile Arg Leu Val Pro His Met Asn Val Ser Ala Val
106    345          350          355          360
107    gaa aaa cag gtg aca cga cat ctt gaa gat gtg ttc tcc aaa aga aat    1377
108    Glu Lys Gln Val Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn
109          365          370          375
110    agt tcc aac aag atg gtt gtt tcc atg act cta gga cta cac ccg tgg    1425
111    Ser Ser Asn Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp
112          380          385          390
113    att gca aat att gat gac acc cag tat ctc gca gca aaa aga gcg atc    1473
114    Ile Ala Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile
115          395          400          405
116    aga aca gtg ttt gga aca gaa cca gat atg atc cgg gat gga tcc acc    1521
117    Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
118    410          415          420
119    att cca att gcc aaa atg ttc cag gag atc gtc cac aag agc gtg gtg    1569
120    Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val Val
121    425          430          435          440
122    cta att ccg ctg gga gct gtt gat gat gga gaa cat tcg cag aat gag    1617
123    Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln Asn Glu
124          445          450          455
125    aaa atc aac agg tgg aac tac ata gag gga acc aaa tta ttt gct gcc    1665
126    Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu Phe Ala Ala
127          460          465          470
128    ttt ttc tta gag atg gcc cag ctc cat taatcacaag aaccttctag    1712
129    Phe Phe Leu Glu Met Ala Gln Leu His
130          475          480
131    tctgatctga tccactgaca gattcacctc cccacatcc ctagacaggg atggaatgta    1772
132    aatatccaga gaatttgggt ctagtatagt acattttccc ttccatttaa aatgtcttgg    1832
133    gatatctgga tcagtaataa aatatttcaa aggcacagat gttggaatg gtttaaggctc    1892
134    cccactgca caccttcctc aagtcatagc tgettgcagc aacttgattt cccaagtcc    1952
135    tgtgcaatag cccaggatt ggattccttc caacctttta gcatatctcc aaccttgcaa    2012
136    tttgattggc ataactcactc cagtttgett tctaggtcct caagtgtctg tgacacataa    2072
137    tcattccatc caatgatcgc ctttgettta ccaactcttc cttttatctt attaataaaa    2132
138    atgttggtct ccaccactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaaaaaa    2192
139    aaaaaaaaaa    2201
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 1631
143 <212> TYPE: DNA

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Output Set: N:\CRF4\01112005\J643836.raw

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144 <213> ORGANISM: Homo sapiens
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: 148..1140
148 <221> NAME/KEY: sig_peptide
149 <222> LOCATION: 148..240
150 <223> OTHER INFORMATION: Von Heijne matrix
151     score 10.0910253445132
152     seq LVLLLVTSPVNA/CL
W--> 153 <400> 2
154     gtctgtgcc gccattgtgc ggcgtgtgct ccctcagagg gttcctgtctg ctgccgggtgc      60
155     cttggaccct cccctcgcgt tctcgttcta ctgccccagg agcccggcggg gtccgggact      120
156     cccgtccgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc      174
157                                     Met Trp Leu Trp Glu Asp Gln Gly Gly
158                                     -30                               -25
159     ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg      222
160     Leu Leu Gly Pro Phe Ser Phe Leu Leu Val Leu Leu Val Thr
161     -20                               -15                               -10
162     cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta      270
163     Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu
164     -5                               1                               5                               10
165     ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag      318
166     Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln
167     15                               20                               25
168     gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc      366
169     Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly
170     30                               35                               40
171     agc cac gac gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct      414
172     Ser His Asp Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala
173     45                               50                               55
174     aag aat gga gca aca ggc gtg gag ttg gac att gag ttt act tct gac      462
175     Lys Asn Gly Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp
176     60                               65                               70
177     ggg att cct gtc tta atg cac gat aac aca gta gat agg acg act gat      510
178     Gly Ile Pro Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp
179     75                               80                               85                               90
180     ggg act ggg cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg      558
181     Gly Thr Gly Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu
182     95                               100                              105
183     aat cct gca gca aac cac aga ctc agg aat gat ttc cct gat gaa aag      606
184     Asn Pro Ala Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys
185     110                              115                              120
186     atc cct acc cta atg gaa gct gtt gca gag tgc cta aac cat aac ctc      654
187     Ile Pro Thr Leu Met Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu
188     125                              130                              135
189     aca atc ttc ttt gat gtc aaa ggc cat gca cac aag gct act gag gct      702
190     Thr Ile Phe Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala
191     140                              145                              150
192     cta aag aaa atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg      750

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Output Set: N:\CRF4\01112005\J643836.raw

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193   Leu Lys Lys Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val
194   155                               160                               165                               170
195   gtc tgt tct ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat      798
196   Val Cys Ser Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp
197                               175                               180                               185
198   cgg gat gta ata aca gca tta act cac aga cct tgg agc cta agc cat      846
199   Arg Asp Val Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His
200                               190                               195                               200
201   aca gga gat ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata      894
202   Thr Gly Asp Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile
203                               205                               210                               215
204   ttt gtt atg atg gac att ttg ctc gat tgg agc atg cat aat atc ttg      942
205   Phe Val Met Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu
206   220                               225                               230
207   tgg tac ctg tgt gga att tca gct ttc ctc atg caa aag gat ttt gta      990
208   Trp Tyr Leu Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val
209   235                               240                               245                               250
210   tcc ccg gcc tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt      1038
211   Ser Pro Ala Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val
212                               255                               260                               265
213   ggt tgg act gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat      1086
214   Gly Trp Thr Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His
215   270                               275                               280
216   ctt ggt tcc agc tat atc act gac agc atg gta gaa gac tgc gaa cct      1134
217   Leu Gly Ser Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro
218   285                               290                               295
219   cac ttc tagactttca cgggtgggacg aaacggggttc agaaactgcc aggggcctca      1190
220   His Phe
221   300
222   tacagggata tcaaaataacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac      1250
223   acaaatgcaa tagttggtca ctgcattttt acctgaacca aagctaaacc cgggtgttgcc      1310
224   accatgcacc atggcatgcc agagttcaac actgttgctc ttgaaaatct ggggtctgaa      1370
225   aaaacgcaca agagcccttg cctgccccta gctgaggcac acaggagagac ccagtgagga      1430
226   taagcacaga ttgaattgta caatttgcag atgcagatgt aaatgcatgg gacatgcatg      1490
227   ataactcaga gttgacattt taaaacttgc cacacttatt tcaaataatt gtactcagct      1550
228   atgttaacat gtactgtaga catcaaactt gtggccatac taataaaatt attaaaagga      1610
229   gcacaaaaaa aaaaaaaaaa a                                1631
231 <210> SEQ ID NO: 3
232 <211> LENGTH: 1245
233 <212> TYPE: DNA
234 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <221> NAME/KEY: CDS
237 <222> LOCATION: 85..906
238 <221> NAME/KEY: sig_peptide
239 <222> LOCATION: 85..135
240 <223> OTHER INFORMATION: Von Heijne matrix
241   score 3.86022363031904
242   seq GFVAALVAGGVAG/VS

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 44,45
Seq#:20; N Pos. 989
Seq#:45; Xaa Pos. 132
Seq#:97; Xaa Pos. 21
Seq#:103; Xaa Pos. 185
Seq#:104; N Pos. 972
Seq#:115; Xaa Pos. 41
Seq#:135; N Pos. 347
Seq#:135; Xaa Pos. 47
Seq#:137; Xaa Pos. 50,51
Seq#:165; N Pos. 1707
Seq#:188; N Pos. 871
Seq#:202; N Pos. 483
Seq#:207; Xaa Pos. 113,114,115
Seq#:210; Xaa Pos. 76
Seq#:220; Xaa Pos. 95
Seq#:253; Xaa Pos. 44,45
Seq#:286; Xaa Pos. 132
Seq#:338; Xaa Pos. 21
Seq#:344; Xaa Pos. 185
Seq#:356; Xaa Pos. 41
Seq#:376; Xaa Pos. 47
Seq#:378; Xaa Pos. 50,51
Seq#:448; Xaa Pos. 113,114,115
Seq#:451; Xaa Pos. 76
Seq#:461; Xaa Pos. 95

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

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Input Set : N:\Crf3\RULE60\10643836.RAW.txt

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L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:318 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:460 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:551 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:650 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:747 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:794 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:896 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:412
L:956 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1005 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:1104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:1170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1238 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:1446 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1449 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:966
L:1516 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:1549 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:1589 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:1641 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1679 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
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L:1896 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:1931 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:2046 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:2142 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:2244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:2281 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:2340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:2425 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37
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L:2770 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41
L:2893 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:3002 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:3106 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:44
L:3191 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:45
L:3225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:654

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10643836.RAW.txt

Output Set: N:\CRF4\01112005\J643836.raw

L:3298 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:46
L:3384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:47
L:3481 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:48
L:3529 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:49
L:3572 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:50
L:6456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97 after pos.:144
L:6752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:923
L:6821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:935
L:7430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:369
L:8386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:310
M:341 Repeated in SeqNo=135
L:8471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:253
M:341 Repeated in SeqNo=137
L:10269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165 after pos.:1691
L:11620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188 after pos.:830
L:12113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202 after pos.:465
L:12300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:207 after pos.:445
L:12472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:210 after pos.:352
L:13039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:220 after pos.:402
L:14556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:253 after pos.:64
L:15877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:286 after pos.:144
L:17668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:338 after pos.:32
L:17827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:344 after pos.:192
L:18185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356 after pos.:64
L:18728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:376 after pos.:64
L:18780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:378 after pos.:48
M:341 Repeated in SeqNo=378
L:20843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:448 after pos.:112
L:20937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:451 after pos.:64
L:21264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:461 after pos.:80